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## SEQUENCE LISTING

<110> Maeda, Masatsugu  
Yaguchi, Noriko

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Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro  
145 150 155 160  
Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg  
165 170 175  
Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg  
180 185 190  
Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr  
195 200 205  
Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp  
210 215 220  
Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Gly Lys  
225 230 235 240  
Leu Leu Pro Ala Ile Pro Val Leu Ser Thr Leu Val  
245 250

<210> 5



<211> 30  
 <212> DNA  
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<220>  
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<400> 5  
 atggaagtca acttcgctaa gaaccgtaag

30

<210> 6  
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<220>  
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<400> 6  
 ccaaacgtac aacctcacgg ggctgcaacc

30

<210> 7  
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<400> 7  
 gtcatagtctc tgcgatgtgc ggtcaaggag

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<210> 8  
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<220>  
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<400> 8  
 agtagcttgc gttcttcctc agctattccc

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<210> 9  
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<220>  
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<400> 9  
 ctttgactcc ttgaccgcac atcgagagc

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<210> 10  
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Q1

<213> Artificial Sequence

<220>

<223> primer

<400> 10

ggttgcagcc ccgtgagggtt gtacgtttgg

30

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 11

atcagatgaa acaggcgcca actcagg

27

<210> 12

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 12

tggtttcaca cggaataatct taggtgg

27

<210> 13

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 13

gcattcagga cagtcaacag taccagc

27

<210> 14

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 14

agctggaatc ctcagggtgg ccactgg

27

<210> 15

<211> 27

<212> DNA

<213> Artificial Sequence

Al

&lt;220&gt;

&lt;223&gt; primer

&lt;400&gt; 15

gcccatacacc agagtagaca ggacggg

27

&lt;210&gt; 16

&lt;211&gt; 2119

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (11)...(1996)

&lt;400&gt; 16

ccccctgatac atg aag ctc tct ccc cag cct tca tgt gtt aac ctg ggg 49

Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly  
1 5 10

atg atg tgg acc tgg gca ctg tgg atg ctc ccc tca ctc tgc aaa ttc 97

Met Met Trp Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe  
15 20 25

agc ctg gca gct ctg cca gct aag cct gag aac att tcc tgt gtc tac 145

Ser Leu Ala Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr  
30 35 40 45

tac tat agg aaa aat tta acc tgc act tgg agt cca gga aag gaa acc 193

Tyr Tyr Arg Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr  
50 55 60

agt tat acc cag tac aca gtt aag aga act tac gct ttt gga gaa aaa 241

Ser Tyr Thr Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys  
65 70 75

cat gat aat tgt aca acc aat agt tct aca agt gaa aat cgt gct tcg 289

His Asp Asn Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser  
80 85 90

tgc tct ttt ttc ctt cca aga ata acg atc cca gat aat tat acc att 337

Cys Ser Phe Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile  
95 100 105

gag gtg gaa gct gaa aat gga gat ggt gta att aaa tct cat atg aca 385

Glu Val Glu Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr  
110 115 120 125

tac tgg aga tta gag aac ata gcg aaa act gaa cca cct aag att ttc 433

Tyr Trp Arg Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe  
130 135 140

cgt gtg aaa cca gtt ttg ggc atc aaa cga atg att caa att gaa tgg 481

Arg Val Lys Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp  
145 150 155

ata aag cct gag ttg gcg cct gtt tca tct gat tta aaa tac aca ctt 529

Al

Ile	Lys	Pro	Glu	Leu	Ala	Pro	Val	Ser	Ser	Asp	Leu	Lys	Tyr	Thr	Leu	
		160					165					170				
cga	ttc	agg	aca	gtc	aac	agt	acc	agc	tgg	atg	gaa	gtc	aac	ttc	gct	577
Arg	Phe	Arg	Thr	Val	Asn	Ser	Thr	Ser	Trp	Met	Glu	Val	Asn	Phe	Ala	
	175					180					185					
aag	aac	cgt	aag	gat	aaa	aac	caa	acg	tac	aac	ctc	acg	ggg	ctg	cag	625
Lys	Asn	Arg	Lys	Asp	Lys	Asn	Gln	Thr	Tyr	Asn	Leu	Thr	Gly	Leu	Gln	
	190				195					200				205		
cct	ttt	aca	gaa	tat	gtc	ata	gct	ctg	cga	tgt	gcg	gtc	aag	gag	tca	673
Pro	Phe	Thr	Glu	Tyr	Val	Ile	Ala	Leu	Arg	Cys	Ala	Val	Lys	Glu	Ser	
			210						215					220		
aag	ttc	tgg	agt	gac	tgg	agc	caa	gaa	aaa	atg	gga	atg	act	gag	gaa	721
Lys	Phe	Trp	Ser	Asp	Trp	Ser	Gln	Glu	Lys	Met	Gly	Met	Thr	Glu	Glu	
		225					230						235			
gaa	gct	cca	tgt	ggc	ctg	gaa	ctg	tgg	aga	gtc	ctg	aaa	cca	gct	gag	769
Glu	Ala	Pro	Cys	Gly	Leu	Glu	Leu	Trp	Arg	Val	Leu	Lys	Pro	Ala	Glu	
		240					245					250				
gcg	gat	gga	aga	agg	cca	gtg	cgg	ttg	tta	tgg	aag	aag	gca	aga	gga	817
Ala	Asp	Gly	Arg	Arg	Pro	Val	Arg	Leu	Leu	Trp	Lys	Lys	Ala	Arg	Gly	
	255					260					265					
gcc	cca	gtc	cta	gag	aaa	aca	ctt	ggc	tac	aac	ata	tgg	tac	tat	cca	865
Ala	Pro	Val	Leu	Glu	Lys	Thr	Leu	Gly	Tyr	Asn	Ile	Trp	Tyr	Tyr	Pro	
	270				275					280					285	
gaa	agc	aac	act	aac	ctc	aca	gaa	aca	atg	aac	act	act	aac	cag	cag	913
Glu	Ser	Asn	Thr	Asn	Leu	Thr	Glu	Thr	Met	Asn	Thr	Thr	Asn	Gln	Gln	
			290						295					300		
ctt	gaa	ctg	cat	ctg	gga	ggc	gag	agc	ttt	tgg	gtg	tct	atg	att	tct	961
Leu	Glu	Leu	His	Leu	Gly	Gly	Glu	Ser	Phe	Trp	Val	Ser	Met	Ile	Ser	
			305					310					315			
tat	aat	tct	ctt	ggg	aag	tct	cca	gtg	gcc	acc	ctg	agg	att	cca	gct	1009
Tyr	Asn	Ser	Leu	Gly	Lys	Ser	Pro	Val	Ala	Thr	Leu	Arg	Ile	Pro	Ala	
		320					325					330				
att	caa	gaa	aaa	tca	ttt	cag	tgc	att	gag	gtc	atg	cag	gcc	tgc	gtt	1057
Ile	Gln	Glu	Lys	Ser	Phe	Gln	Cys	Ile	Glu	Val	Met	Gln	Ala	Cys	Val	
	335					340					345					
gct	gag	gac	cag	cta	gtg	gtg	aag	tgg	caa	agc	tct	gct	cta	gac	gtg	1105
Ala	Glu	Asp	Gln	Leu	Val	Val	Lys	Trp	Gln	Ser	Ser	Ala	Leu	Asp	Val	
	350				355					360				365		
aac	act	tgg	atg	att	gaa	tgg	ttt	ccg	gat	gtg	gac	tca	gag	ccc	acc	1153
Asn	Thr	Trp	Met	Ile	Glu	Trp	Phe	Pro	Asp	Val	Asp	Ser	Glu	Pro	Thr	
			370						375				380			
acc	ctt	tcc	tgg	gaa	tct	gtg	tct	cag	gcc	acg	aac	tgg	acg	atc	cag	1201
Thr	Leu	Ser	Trp	Glu	Ser	Val	Ser	Gln	Ala	Thr	Asn	Trp	Thr	Ile	Gln	

Q1

385										390										395									
caa	gat	aaa	tta	aaa	cct	ttc	tgg	tgc	tat	aac	atc	tct	gtg	tat	cca														
Gln	Asp	Lys	Leu	Lys	Pro	Phe	Trp	Cys	Tyr	Asn	Ile	Ser	Val	Tyr	Pro														
		400					405					410																	
atg	ttg	cat	gac	aaa	gtt	ggc	gag	cca	tat	tcc	atc	cag	gct	tat	gcc														
Met	Leu	His	Asp	Lys	Val	Gly	Glu	Pro	Tyr	Ser	Ile	Gln	Ala	Tyr	Ala														
		415				420					425																		
aaa	gaa	ggc	gtt	cca	tca	gaa	ggg	cct	gag	acc	aag	gtg	gag	aac	att														
Lys	Glu	Gly	Val	Pro	Ser	Glu	Gly	Pro	Glu	Thr	Lys	Val	Glu	Asn	Ile														
430					435					440					445														
ggc	gtg	aag	acg	gtc	acg	atc	aca	tgg	aaa	gag	att	ccc	aag	agt	gag														
Gly	Val	Lys	Thr	Val	Thr	Ile	Thr	Trp	Lys	Glu	Ile	Pro	Lys	Ser	Glu														
				450					455				460																
aga	aag	ggg	atc	atc	tgc	aac	tac	acc	atc	ttt	tac	caa	gct	gaa	ggg														
Arg	Lys	Gly	Ile	Ile	Cys	Asn	Tyr	Thr	Ile	Phe	Tyr	Gln	Ala	Glu	Gly														
			465				470					475																	
gga	aaa	gga	ttc	tcc	aag	aca	gtc	aat	tcc	agc	atc	ttg	cag	tac	ggc														
Gly	Lys	Gly	Phe	Ser	Lys	Thr	Val	Asn	Ser	Ser	Ile	Leu	Gln	Tyr	Gly														
		480				485					490																		
ctg	gag	tcc	ctg	aaa	cga	aag	acc	tct	tac	att	gtt	cag	gtc	atg	gcc														
Leu	Glu	Ser	Leu	Lys	Arg	Lys	Thr	Ser	Tyr	Ile	Val	Gln	Val	Met	Ala														
		495				500					505																		
agc	acc	agt	gct	ggg	gga	acc	aac	ggg	acc	agc	ata	aat	ttc	aag	aca														
Ser	Thr	Ser	Ala	Gly	Gly	Thr	Asn	Gly	Thr	Ser	Ile	Asn	Phe	Lys	Thr														
510					515					520					525														
ttg	tca	ttc	agt	gtc	ttt	gag	att	atc	ctc	ata	act	tct	ctg	att	ggg														
Leu	Ser	Phe	Ser	Val	Phe	Glu	Ile	Ile	Leu	Ile	Thr	Ser	Leu	Ile	Gly														
				530					535				540																
gga	ggc	ctt	ctt	att	ctc	att	atc	ctg	aca	gtg	gca	tat	ggg	ctc	aaa														
Gly	Gly	Leu	Leu	Ile	Leu	Ile	Ile	Leu	Thr	Val	Ala	Tyr	Gly	Leu	Lys														
				545				550				555																	
aaa	ccc	aac	aaa	ttg	act	cat	ctg	tgt	tgg	ccc	acc	gtt	ccc	aac	cct														
Lys	Pro	Asn	Lys	Leu	Thr	His	Leu	Cys	Trp	Pro	Thr	Val	Pro	Asn	Pro														
		560					565					570																	
gct	gaa	agt	agt	ata	gcc	aca	tgg	cat	gga	gat	gat	ttc	aag	gat	aag														
Ala	Glu	Ser	Ser	Ile	Ala	Thr	Trp	His	Gly	Asp	Asp	Phe	Lys	Asp	Lys														
		575				580					585																		
cta	aac	ctg	aag	gag	tct	gat	gac	tct	gtg	aac	aca	gaa	gac	agg	atc														
Leu	Asn	Leu	Lys	Glu	Ser	Asp	Asp	Ser	Val	Asn	Thr	Glu	Asp	Arg	Ile														
590					595				600						605														
tta	aaa	cca	tgt	tcc	acc	ccc	agt	gac	aag	ttg	gtg	att	gac	aag	ttg														
Leu	Lys	Pro	Cys	Ser	Thr	Pro	Ser	Asp	Lys	Leu	Val	Ile	Asp	Lys	Leu														
				610					615						620														

Q1

gtg gtg aac ttt ggg aat gtt ctg caa gaa att ttc aca gat gaa gcc 1921  
 Val Val Asn Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala  
 625 630 635

aga acg ggt cag gaa aac aat tta gga ggg gaa aag aat ggg act aga 1969  
 Arg Thr Gly Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg  
 640 645 650

att ctg tct tcc tgc cca act tca ata taagtgtgga ctaaaatgcg 2016  
 Ile Leu Ser Ser Cys Pro Thr Ser Ile  
 655 660

agaaagggtgt cctgtggtct atgcaaatta gaaaggacat gcagagtttt ccaactagga 2076  
 agactgaatc tgtggcccca agagaaccat ctccgaagac tgg 2119

<210> 17

<211> 662

<212> PRT

<213> Homo sapiens

<400> 17

Met Lys Leu Ser Pro Gln Pro Ser Cys Val Asn Leu Gly Met Met Trp  
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 Thr Trp Ala Leu Trp Met Leu Pro Ser Leu Cys Lys Phe Ser Leu Ala  
 20 25 30  
 Ala Leu Pro Ala Lys Pro Glu Asn Ile Ser Cys Val Tyr Tyr Tyr Arg  
 35 40 45  
 Lys Asn Leu Thr Cys Thr Trp Ser Pro Gly Lys Glu Thr Ser Tyr Thr  
 50 55 60  
 Gln Tyr Thr Val Lys Arg Thr Tyr Ala Phe Gly Glu Lys His Asp Asn  
 65 70 75 80  
 Cys Thr Thr Asn Ser Ser Thr Ser Glu Asn Arg Ala Ser Cys Ser Phe  
 85 90 95  
 Phe Leu Pro Arg Ile Thr Ile Pro Asp Asn Tyr Thr Ile Glu Val Glu  
 100 105 110  
 Ala Glu Asn Gly Asp Gly Val Ile Lys Ser His Met Thr Tyr Trp Arg  
 115 120 125  
 Leu Glu Asn Ile Ala Lys Thr Glu Pro Pro Lys Ile Phe Arg Val Lys  
 130 135 140  
 Pro Val Leu Gly Ile Lys Arg Met Ile Gln Ile Glu Trp Ile Lys Pro  
 145 150 155 160  
 Glu Leu Ala Pro Val Ser Ser Asp Leu Lys Tyr Thr Leu Arg Phe Arg  
 165 170 175  
 Thr Val Asn Ser Thr Ser Trp Met Glu Val Asn Phe Ala Lys Asn Arg  
 180 185 190  
 Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Phe Thr  
 195 200 205  
 Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe Trp  
 210 215 220  
 Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Ala Pro  
 225 230 235 240  
 Cys Gly Leu Glu Leu Trp Arg Val Leu Lys Pro Ala Glu Ala Asp Gly  
 245 250 255  
 Arg Arg Pro Val Arg Leu Leu Trp Lys Lys Ala Arg Gly Ala Pro Val  
 260 265 270  
 Leu Glu Lys Thr Leu Gly Tyr Asn Ile Trp Tyr Tyr Pro Glu Ser Asn

275 280 285  
 Thr Asn Leu Thr Glu Thr Met Asn Thr Thr Asn Gln Gln Leu Glu Leu  
 290 295 300  
 His Leu Gly Gly Glu Ser Phe Trp Val Ser Met Ile Ser Tyr Asn Ser  
 305 310 315 320  
 Leu Gly Lys Ser Pro Val Ala Thr Leu Arg Ile Pro Ala Ile Gln Glu  
 325 330 335  
 Lys Ser Phe Gln Cys Ile Glu Val Met Gln Ala Cys Val Ala Glu Asp  
 340 345 350  
 Gln Leu Val Val Lys Trp Gln Ser Ser Ala Leu Asp Val Asn Thr Trp  
 355 360 365  
 Met Ile Glu Trp Phe Pro Asp Val Asp Ser Glu Pro Thr Thr Leu Ser  
 370 375 380  
 Trp Glu Ser Val Ser Gln Ala Thr Asn Trp Thr Ile Gln Gln Asp Lys  
 385 390 395 400  
 Leu Lys Pro Phe Trp Cys Tyr Asn Ile Ser Val Tyr Pro Met Leu His  
 405 410 415  
 Asp Lys Val Gly Glu Pro Tyr Ser Ile Gln Ala Tyr Ala Lys Glu Gly  
 420 425 430  
 Val Pro Ser Glu Gly Pro Glu Thr Lys Val Glu Asn Ile Gly Val Lys  
 435 440 445  
 Thr Val Thr Ile Thr Trp Lys Glu Ile Pro Lys Ser Glu Arg Lys Gly  
 450 455 460  
 Ile Ile Cys Asn Tyr Thr Ile Phe Tyr Gln Ala Glu Gly Gly Lys Gly  
 465 470 475 480  
 Phe Ser Lys Thr Val Asn Ser Ser Ile Leu Gln Tyr Gly Leu Glu Ser  
 485 490 495  
 Leu Lys Arg Lys Thr Ser Tyr Ile Val Gln Val Met Ala Ser Thr Ser  
 500 505 510  
 Ala Gly Gly Thr Asn Gly Thr Ser Ile Asn Phe Lys Thr Leu Ser Phe  
 515 520 525  
 Ser Val Phe Glu Ile Ile Leu Ile Thr Ser Leu Ile Gly Gly Gly Leu  
 530 535 540  
 Leu Ile Leu Ile Ile Leu Thr Val Ala Tyr Gly Leu Lys Lys Pro Asn  
 545 550 555 560  
 Lys Leu Thr His Leu Cys Trp Pro Thr Val Pro Asn Pro Ala Glu Ser  
 565 570 575  
 Ser Ile Ala Thr Trp His Gly Asp Asp Phe Lys Asp Lys Leu Asn Leu  
 580 585 590  
 Lys Glu Ser Asp Asp Ser Val Asn Thr Glu Asp Arg Ile Leu Lys Pro  
 595 600 605  
 Cys Ser Thr Pro Ser Asp Lys Leu Val Ile Asp Lys Leu Val Val Asn  
 610 615 620  
 Phe Gly Asn Val Leu Gln Glu Ile Phe Thr Asp Glu Ala Arg Thr Gly  
 625 630 635 640  
 Gln Glu Asn Asn Leu Gly Gly Glu Lys Asn Gly Thr Arg Ile Leu Ser  
 645 650 655  
 Ser Cys Pro Thr Ser Ile  
 660

<210> 18  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> primer

<400> 18  
cccctgatac atgaagctct ctccccagcc

30

<210> 19  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 19  
ccagtcttcg gagatgggtc tcttggggcc

30

<210> 20  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> primer

<400> 20  
ctgtgtaagt accaattggt cccaggc

27

<210> 21  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> exemplary motif

<221> misc\_feature  
<222> 7-9  
<223> n = a, t, g, or c

<400> 21  
tggagynnnt ggagy

15

<210> 22  
<211> 5  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> exemplary motif

<221> VARIANT  
<222> 3  
<223> Xaa = any amino acid

<400> 22  
Trp Ser Xaa Trp Ser  
1 5

61



<210> 23  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<400> 23  
 Tyr Thr Val Gln Val Arg  
 1 5

<210> 24  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<400> 24  
 Tyr Glu Ala Arg Val Arg  
 1 5

<210> 25  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<400> 25  
 Tyr Ser Leu Gln Leu Arg  
 1 5

<210> 26  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> exemplary motif

<221> VARIANT  
 <222> 3-8  
 <223> Xaa = any amino acid

<400> 26  
 Ala Arg Xaa Xaa Xaa Xaa Xaa Xaa Gly Thr  
 1 5 10

<210> 27  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

Q1

<220>  
<223> exemplary motif

<221> VARIANT  
<222> 3-8  
<223> Xaa = any amino acid

<400> 27  
Val Gln Xaa Xaa Xaa Xaa Xaa Xaa Gly Tyr  
1 5 10

<210> 28  
<211> 10  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> exemplary motif  
  
<221> VARIANT  
<222> 3-8  
<223> Xaa = any amino acid

<400> 28  
Cys Lys Xaa Xaa Xaa Xaa Xaa Xaa Gly Ile  
1 5 10

<210> 29  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> exemplary motif

<400> 29  
Trp Ser Glu Trp Ser Pro  
1 5

<210> 30  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> exemplary motif

<400> 30  
Trp Ser Asp Trp Ser Glu  
1 5

<210> 31  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>

Q1

<223> exemplary motif

<400> 31

Trp Ser Pro Trp Ser Gln  
1 5

<210> 32

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> exemplary motif

<400> 32

Tyr Val Ile Ala Leu Arg  
1 5

<210> 33

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> exemplary motif

<400> 33

Trp Ser Asp Trp Ser  
1 5

<210> 34

<211> 459

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (211)...(399)

<221> misc\_feature

<222> 281, 376, 420

<223> n = A,T,C or G

<400> 34

ttggtggttc atggtgatgt tctatatctg tgtaagtacc aattggtccc aggcacatat	60
ggaagtctgt taataaaaat gatatatattt aaaatttgat ttagagtgtt actagttcta	120
aaaatgtaaa agtacactag gtagtgaaga ggaaaatggg aggataacgt gtggtctcca	180
tttcagttta cgattgtctc tgtctttag atg gaa gtc aac ttc gct aag aac	234
Met Glu Val Asn Phe Ala Lys Asn	
1 5	

cgt aag gat aaa aac caa acg tac aac ctc acg ggg ctg caa cct tnt	282
Arg Lys Asp Lys Asn Gln Thr Tyr Asn Leu Thr Gly Leu Gln Pro Xaa	
10 15 20	

aca gaa tat gtc ata gct ctg cga tgt gcg gtc aag gag tca aag ttc	330
Thr Glu Tyr Val Ile Ala Leu Arg Cys Ala Val Lys Glu Ser Lys Phe	

Q1

25 30 35 40

tgg agt gac tgg agc caa gaa aaa atg gga atg act gag gaa gaa ngc 378  
 Trp Ser Asp Trp Ser Gln Glu Lys Met Gly Met Thr Glu Glu Glu Xaa  
 45 50 55

aag cta ctt cct gcg att ccc gtctgtctg ctctggtgta nggctgctct 429  
 Lys Leu Leu Pro Ala Ile Pro  
 60

gcgctaaact tgggtggtgtc tgcaccaccg 459

<210> 35  
 <211> 63  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> VARIANT  
 <222> 24, 54  
 <223> Xaa = any amino acid

<400> 35  
 Met Glu Val Asn Phe Ala Lys Asn Arg Lys Asp Lys Asn Gln Thr Tyr  
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 Asn Leu Thr Gly Leu Gln Pro Xaa Thr Glu Tyr Val Ile Ala Leu Arg  
 20 25 30  
 Cys Ala Val Lys Glu Ser Lys Phe Trp Ser Asp Trp Ser Gln Glu Lys  
 35 40 45  
 Met Gly Met Thr Glu Glu Glu Xaa Lys Leu Leu Pro Ala Ile Pro  
 50 55 60

<210> 36  
 <211> 42  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Ser Phe Thr Val Gln Asp Leu Lys Pro Phe Thr Glu Tyr Val Phe Arg  
 1 5 10 15  
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 Ala Gly Ile Trp Ser Glu Trp Ser His Pro Thr Ala Ala Ser Thr Pro  
 35 40 45  
 Arg Ser Gly  
 50

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